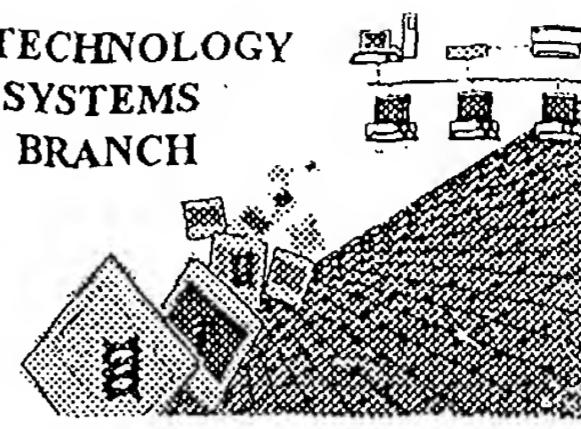


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/602,544
Source: 1Ew0
Date Processed by STIC: 12/20/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
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<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

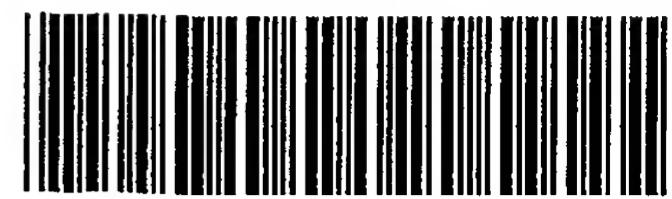
Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

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1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 10/08/03



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/602,544

DATE: 12/20/2003
TIME: 14:20:51

Input Set : A:\SEQLIST.txt
Output Set: N:\CRF4\12182003\J602544.raw

3 <110> APPLICANT: . Li-fang Liang
 5 <120> TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR PROMOTER AND USES
 6 THEREFOR
 8 <130> FILE REFERENCE: MTN-027DV1CN
 10 <140> CURRENT APPLICATION NUMBER: 10/602,544
 11 <141> CURRENT FILING DATE: 2003-06-23
 13 <150> PRIOR APPLICATION NUMBER: US 09/632,879
 14 <151> PRIOR FILING DATE: 2000-08-04
 16 <150> PRIOR APPLICATION NUMBER: 60/092,865
 17 <151> PRIOR FILING DATE: 1998-07-15
 19 <150> PRIOR APPLICATION NUMBER: 60/123,270
 20 <151> PRIOR FILING DATE: 1999-03-08
 22 <150> PRIOR APPLICATION NUMBER: 09/354,409
 23 <151> PRIOR FILING DATE: 1999-07-15
 25 <160> NUMBER OF SEQ ID NOS: 9
 27 <170> SOFTWARE: PatentIn Ver. 2.0

*Doc No. Comply
Corrected Unique Number*

ERRORED SEQUENCES

133 <210> SEQ ID NO: 9
 134 <211> LENGTH: 159
 135 <212> TYPE: DNA
 136 <213> ORGANISM: Gallus gallus
 138 <400> SEQUENCE: 9
 139 gaagccagga tataaatcag ttcacccttg gctgtaacca aatgctgtct agtgacttgt 60
 140 gatcgacagg gctttaacct ctgacagacta gattcattgt tgggacaaca accaatcg 120
 141 gttttgacg acatgagcct aatcaaagtt ggagtataa 159

E--> 144 (1)

delete

see p.2 for more errors

10/602,544

2

<210> 5
<211> 799
<212> DNA
<213> Gallus gallus

<220>

<223> AT POSITIONS

9, 30, 32, 50, 55, 92, 114, 146, 149, 151, 154, 158, AND 170 N

CAN BE ANY NUCLEOTIDE

<400> 5

ttcggtatnt aatttgctgc ccaggatttn gntgacaaag gcaaactggn ttaanttaat 60
agggtccaca cttcagtaat gaattttgat antaaaggc ccaatagtta gcanttata 120
tcacacgtga acaaaatgtt tattcntgnt nacntagnac ntatcaggaa aacctatcat 180
gattttctga aatctgagct gcttaatgca cgtgaactgt tgaacagcat ggattcctcg 240
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aaaagagagc tctgcctcaa ttcatagtcc aactatgcgt tcagtgtata tttaagaatg 420
atagtgtgt ctccagcac tgctgccat agtacttgaa aatatacct ttcatgtatgt 480
gaagacgtat ccttacgaa gccaccatat aaatcagtcc acccttggct gtaaccaa 540
gctgtctagt gacttgtat cgacagggct ttaacctctg acagcttagat tcattgttgg 600
gacaacaacc aatcgctgg tttgacgaca tgagccta at caaagttgga gtataaaagc 660
ccccttggca tatataaggc acaccagtgt ggcaagccgt ctctcagatt gcatttgctg 720
tcacggatct gtttagaact gaaagaaaag gggaaaggaa gaggggggaa aaaagggcaa 780
aaagctgcag tgactgtaa 799

161 (^a is at location 170)

FYI: Per 1.823

of sequence
Rules, list
the locations
of n or
Xaa on

<222> list

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/602,544

DATE: 12/20/2003
TIME: 14:20:52

Input Set : A:\SEQLIST.txt
Output Set: N:\CRF4\12182003\J602544.raw

Use of n's or Xaa's (NEW RULES) :

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:5; N Pos. 9,30,32,50,55,92,114,146,149,151,154,158,161

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/602,544

DATE: 12/20/2003
TIME: 14:20:52

Input Set : A:\SEQLIST.txt
Output Set: N:\CRF4\12182003\J602544.raw

L:88 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:88 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:144 M:254 E: No. of Bases conflict, this line has no nucleotides.